What is claimed is

1. An oligonucleotide library for detecting messenger RNAs that populate a transcriptome, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants.

2. The oligonucleotide library of claim 1, wherein said transcriptome is a human transcriptome.

3. The oligonucleotide library of claim 1, wherein said transcriptome is a rat transcriptome.

4. The oligonucleotide library of claim 1, wherein said transcriptome is a mouse transcriptome.

5. An oligonucleotide library for detecting messenger RNAs that populate a sub transcriptome of a tissue origin, wherein the sub transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a sub genome of the tissue origin, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the sub genome, wherein at least one transcription unit of the sub genome encodes one or more messenger RNA splice variants.

6. An oligonucleotide library for detecting messenger RNAs that populate a sub transcriptome of a pathological tissue origin, wherein the sub

transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a sub genome of the pathological tissue origin, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the sub genome, wherein at least one transcription unit of the sub genome encodes one or more messenger RNA splice variants.

7. The oligonucleotide library of claim 6, wherein said pathological tissue origin is cancer tissue.

8. An oligonucleotide library for detecting messenger RNAs that populate a sub transcriptome of a developmental stage, wherein the sub transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a sub genome of the developmental stage, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the sub genome, wherein at least one transcription unit of the sub genome encodes one or more messenger RNA splice variants.

9. An oligonucleotide library for detecting messenger RNAs that populate a transcriptome of patients suffering from a disorder, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome of patients suffering from the disorder, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants.

10. The oligonucleotide library of claim 9, wherein said disorder is cancer.

11. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 1 or a subset thereof.

12. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 5 or a subset thereof.

13. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 6 or a subset thereof.

14. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 8 or a subset thereof.

15. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 9 or a subset thereof.

16. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 1 or a subset thereof.

17. The method of claim 16, wherein said hybridization signals are obtained from a nucleotide chip.

18. The method of claim 16, wherein said hybridization signals are obtained from an electrophoresis gel.

19. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 5 or a subset thereof.

20. The method of claim 19, wherein said hybridization signals are obtained from a nucleotide chip.

21. The method of claim 19, wherein said hybridization signals are obtained from an electrophoresis gel.

22. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 6 or a subset thereof.

23. The method of claim 22, wherein said hybridization signals are obtained from a nucleotide chip.

24. The method of claim 22, wherein said hybridization signals are obtained from an electrophoresis gel.

25. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 8 or a subset thereof.

26. The method of claim 25, wherein said hybridization signals are obtained from a nucleotide chip.

27. The method of claim 25, wherein said hybridization signals are obtained from an electrophoresis gel.

28. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 9 or a subset thereof.

29. An oligonucleotide library for detecting messenger RNAs that populate a transcriptome, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to one or a subset of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants.

30. The oligonucleotide library of claim 29, wherein said transcriptome is a human transcriptome.

31. The oligonucleotide library of claim 29, wherein said transcriptome is rat transcriptome.

32. The oligonucleotide library of claim 29, wherein said transcriptome is a mouse transcriptome.

33. An oligonucleotide library for detecting messenger RNAs that populate a sub transcriptome of a tissue origin, wherein the sub transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a sub genome of the tissue origin, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to one or a subset of messenger RNAs transcribed from a given transcription unit of the sub genome, wherein at least one transcription unit of the sub genome encodes one or more messenger RNA splice variants.

34. An oligonucleotide library for detecting messenger RNAs that populate a sub transcriptome of a pathological tissue origin, wherein the sub transcriptome comprises messenger RNAs transcribed from a multiplicity of

transcription units that populate a sub genome of the pathological tissue origin, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to one or a subset of messenger RNAs transcribed from a given transcription unit of the sub genome, wherein at least one transcription unit of the sub genome encodes one or more messenger RNA splice variants.

35. The oligonucleotide library of claim 34, wherein said pathological tissue origin is cancer tissue.

36. An oligonucleotide library for detecting messenger RNAs that populate a sub transcriptome of a developmental stage, wherein the sub transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a sub genome of the developmental stage, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to one or a subset of messenger RNAs transcribed from a given transcription unit of the sub genome, wherein at least one transcription unit of the sub genome encodes one or more messenger RNA splice variants.

37. An oligonucleotide library for detecting messenger RNAs that populate a transcriptome of patients suffering from a disorder, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome of patients suffering from the disorder, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to one or a subset of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants.

38. The oligonucleotide library of claim 37, wherein said disorder is cancer.

39. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 29 or a subset thereof.

40. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 33 or a subset thereof.

41. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 34 or a subset thereof.

42. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 36 or a subset thereof.

43. A DNA microarray having spotted thereon a plurality of oligonucleotide sequences, wherein said plurality is provided by the oligonucleotide library of claim 37 or a subset thereof.

44. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 29 or a subset thereof.

45. The method of claim 44, wherein said hybridization signals are obtained from a nucleotide chip.

46. The method of claim 44, wherein said hybridization signals are obtained from an electrophoresis gel.

47. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 33 or a subset thereof.

48. The method of claim 47, wherein said hybridization signals are obtained from a nucleotide chip.

49. The method of claim 47, wherein said hybridization signals are obtained from an electrophoresis gel.

50. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 34 or a subset thereof.

51. The method of claim 50, wherein said hybridization signals are obtained from a nucleotide chip.

52. The method of claim 50, wherein said hybridization signals are obtained from an electrophoresis gel.

53. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 36 or a subset thereof.

54. The method of claim 53, wherein said hybridization signals are obtained from a nucleotide chip.

55. The method of claim 53, wherein said hybridization signals are obtained from an electrophoresis gel.

56. A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 37 or a subset thereof.

57. The method of claim 56, wherein said hybridization signals are obtained from a nucleotide chip.

58. The method of claim 56, wherein said hybridization signals are obtained from an electrophoresis gel.

59. A double stranded RNA molecule based on an oligonucleotide selected from an oligonucleotide library for detecting messenger RNAs that populate a transcriptome, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants, wherein

the double-stranded RNA molecule comprises no more than 30 basepairs, wherein the double-stranded RNA molecule can interfere with translation of an mRNA.

60. An antisense molecule based on an oligonucleotide selected from an oligonucleotide library for detecting messenger RNAs that populate a transcriptome, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants, wherein

the antisense molecule comprises no more than 30 bases, wherein the double-stranded RNA molecule can interfere with translation of an mRNA.